

18199CB



## SEQUENCE LISTING

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Conn, Gregory L.  
Thomas, Jr., Kenneth A.

<120> VASCULAR ENDOTHELIAL CELL GROWTH FACTOR  
II

<130> 18199CB

<140> US 10/071,370

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<150> 09/326,879

<151> 1999-06-07

<150> 09/038,199

<151> 1998-03-10

<150> 08/299,185

<151> 1994-08-31

<150> 08/000,834

<151> 1993-01-05

<150> 07/586,638

<151> 1990-09-21

<160> 29

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<210> 1

<211> 577

<212> DNA

<213> rat

<220>

<221> CDS

<222> (5)...(577)

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1 5 10 15	

ctg tac ctc cac cat gcc aag tgg tcc cag gct gca ccc acg aca gaa	97
Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu	
20 25 30	

ggg gag cag aaa gcc cat gaa gtg gtg aag ttc atg gac gtc tac cag	145
Gly Glu Gln Lys Ala His Glu Val Val Lys Phe Met Asp Val Tyr Gln	
35 40 45	

cgc agc tat tgc cgt ccg att gag acc ctg gtg gac atc ttc cag gag 193  
 Arg Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
           50                          55                          60

tac ccc gat gag ata gag tat atc ttc aag ccg tcc tgt gtg ccc cta 241  
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
           65                          70                          75

atg cgg tgt gcg ggc tgc tgc aat gat gaa gcc ctg gag tgc gtg ccc 289  
 Met Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro  
           80                          85                          90                          95

acg tcg gag agc aac gtc act atg cag atc atg cgg atc aaa cct cac 337  
 Thr Ser Glu Ser Asn Val Thr Met Gln Ile Met Arg Ile Lys Pro His  
                           100                          105                          110

caa agc cag cac ata gga gag atg agc ttc ctg cag cat agc aga tgt 385  
 Gln Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys  
                           115                          120                          125

gaa tgc aga cca aag aaa gat aga aca aag cca gaa aat cac tgt gag 433  
 Glu Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Asn His Cys Glu  
                           130                          135                          140

cct tgt tca gag cgg aga aag cat ttg ttt gtc caa gat ccg cag acg 481  
 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr  
                           145                          150                          155

tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag 529  
 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln  
                           160                          165                          170                          175

ctt gag tta aac gaa cgt act tgc aga tgt gac aag cca agg cgg tga 577  
 Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg \*  
                           180                          185                          190

<210> 2  
 <211> 190  
 <212> PRT  
 <213> rat

<400> 2  
 Met Asn Phe Leu Leu Ser Trp Val His Trp Thr Leu Ala Leu Leu Leu  
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 Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Thr Thr Glu Gly  
           20                          25                          30  
 Glu Gln Lys Ala His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg  
           35                          40                          45  
 Ser Tyr Cys Arg Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr  
   50                          55                          60  
 Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met  
   65                          70                          75                          80  
 Arg Cys Ala Gly Cys Cys Asn Asp Glu Ala Leu Glu Cys Val Pro Thr  
           85                          90                          95

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Ser Glu Ser Asn Val Thr Met Gln Ile Met Arg Ile Lys Pro His Gln
      100      105      110
Ser Gln His Ile Gly Glu Met Ser Phe Leu Gln His Ser Arg Cys Glu
      115      120      125
Cys Arg Pro Lys Lys Asp Arg Thr Lys Pro Glu Asn His Cys Glu Pro
      130      135      140
Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys
      145      150      155      160
Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu
      165      170      175
Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg
      180      185      190

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&lt;210&gt; 3

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; rat

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(477)

&lt;400&gt; 3

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atg ctg gcc atg aag ctg ttc act tgc ttc ttg cag gtc cta gct ggg      48
Met Leu Ala Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly
  1              5              10              15

ttg gct gtg cac tcc cag ggg gcc ctg tct gct ggg aac aac tca aca      96
Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr
      20              25              30

gaa atg gaa gtg gtg cct ttc aat gaa gtg tgg ggc cgc agc tac tgc      144
Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys
      35              40              45

cgg cca atg gag aag ctg gtg tac att gca gat gaa cac cct aat gaa      192
Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu
      50              55              60

gtg tct cat ata ttc agt ccg tca tgt gtc ctt ctg agt cgc tgt agt      240
Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser
      65              70              75              80

ggc tgc tgt ggt gac gag ggt ctg cac tgt gtg gcg cta aag aca gcc      288
Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala
      85              90              95

aac atc act atg cag atc tta aag att ccc ccc aat cgg gat cca cat      336
Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His
      100              105              110

tcc tac gtg gag atg aca ttc tct cag gat gta ctc tgc gaa tgc agg      384
Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg
      115              120              125

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cct att ctg gag acg aca aag gca gaa agg agg aaa acc aag ggg aag 432  
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg Lys Thr Lys Gly Lys  
 130 135 140

agg aag caa agc aaa acc cca cag act gag gaa ccc cac ctg tga 477  
 Arg Lys Gln Ser Lys Thr Pro Gln Thr Glu Glu Pro His Leu \*  
 145 150 155

<210> 4  
 <211> 158  
 <212> PRT  
 <213> rat

<400> 4  
 Met Leu Ala Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly  
 1 5 10 15  
 Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr  
 20 25 30  
 Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys  
 35 40 45  
 Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu  
 50 55 60  
 Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser  
 65 70 75 80  
 Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala  
 85 90 95  
 Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His  
 100 105 110  
 Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg  
 115 120 125  
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg Arg Lys Thr Lys Gly Lys  
 130 135 140  
 Arg Lys Gln Ser Lys Thr Pro Gln Thr Glu Glu Pro His Leu  
 145 150 155

<210> 5  
 <211> 417  
 <212> DNA  
 <213> rat

<220>  
 <221> CDS  
 <222> (1)...(417)

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 1 5 10 15

ttg gct gtg cac tcc cag ggg gcc ctg tct gct ggg aac aac tca aca 96  
 Leu Ala Val His Ser Gln Gly Ala Leu Ser Ala Gly Asn Asn Ser Thr  
 20 25 30

gaa atg gaa gtg gtg cct ttc aat gaa gtg tgg ggc cgc agc tac tgc 144  
 Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys  
           35                          40                          45

cgg cca atg gag aag ctg gtg tac att gca gat gaa cac cct aat gaa 192  
 Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu  
           50                          55                          60

gtg tct cat ata ttc agt ccg tca tgt gtc ctt ctg agt cgc tgt agt 240  
 Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser  
           65                          70                          75                          80

ggc tgc tgt ggt gac gag ggt ctg cac tgt gtg gcg cta aag aca gcc 288  
 Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala  
                           85                          90                          95

aac atc act atg cag atc tta aag att ccc ccc aat cgg gat cca cat 336  
 Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His  
                           100                          105                          110

tcc tac gtg gag atg aca ttc tct cag gat gta ctc tgc gaa tgc agg 384  
 Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg  
           115                          120                          125

cct att ctg gag acg aca aag gca gaa agg taa 417  
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg \*  
           130                          135

<210> 6  
 <211> 138  
 <212> PRT  
 <213> rat

<400> 6  
 Met Leu Ala Met Lys Leu Phe Thr Cys Phe Leu Gln Val Leu Ala Gly  
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           20                          25                          30  
 Glu Met Glu Val Val Pro Phe Asn Glu Val Trp Gly Arg Ser Tyr Cys  
           35                          40                          45  
 Arg Pro Met Glu Lys Leu Val Tyr Ile Ala Asp Glu His Pro Asn Glu  
           50                          55                          60  
 Val Ser His Ile Phe Ser Pro Ser Cys Val Leu Leu Ser Arg Cys Ser  
           65                          70                          75                          80  
 Gly Cys Cys Gly Asp Glu Gly Leu His Cys Val Ala Leu Lys Thr Ala  
                           85                          90                          95  
 Asn Ile Thr Met Gln Ile Leu Lys Ile Pro Pro Asn Arg Asp Pro His  
           100                          105                          110  
 Ser Tyr Val Glu Met Thr Phe Ser Gln Asp Val Leu Cys Glu Cys Arg  
           115                          120                          125  
 Pro Ile Leu Glu Thr Thr Lys Ala Glu Arg  
           130                          135

<210> 7  
 <211> 14

&lt;212&gt; PRT

&lt;213&gt; rat

&lt;400&gt; 7

Ala Pro Thr Thr Glu Gly Glu Gln Lys Ala His Glu Val Val  
 1 5 10

&lt;210&gt; 8

&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; rat

&lt;220&gt;

&lt;221&gt; MOD\_RES

&lt;222&gt; (7)...(7)

&lt;223&gt; Xaa = Unknown

&lt;400&gt; 8

Ala Leu Ser Ala Gly Asn Xaa Ser Thr Glu Met Glu Val Val Pro Phe  
 1 5 10 15  
 Asn Glu Val

&lt;210&gt; 9

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide

&lt;221&gt; modified\_base

&lt;222&gt; (0)...(0)

<223> n = t,c,g,a  
 y=t,c

&lt;400&gt; 9

tttgtcgact yatggaygtn tayca

25

&lt;210&gt; 10

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide

&lt;221&gt; modified\_base

&lt;222&gt; (0)...(0)

<223> n = t,c,g,a  
 y = t,c  
 r = a,g

&lt;400&gt; 10

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32

<210> 11  
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 <212> DNA  
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 <210> 12  
 <211> 25  
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 <223> oligonucleotide  
  
 <400> 12  
 tttgtcgact cagagcggag aaagc 25  
  
 <210> 13  
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 <212> DNA  
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 <223> oligonucleotide  
  
 <400> 13  
 tttgtcgacg aaaatcactg tgagc 25  
  
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 <212> DNA  
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 <223> oligonucleotide  
  
 <400> 14  
 gactcgagtc gacatcg 17  
  
 <210> 15  
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 <212> DNA  
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 <223> oligonucleotide  
  
 <400> 15  
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<210> 16  
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<220>  
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<400> 16  
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28

<210> 17  
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 <212> DNA  
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 <223> oligonucleotide

<400> 17  
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18

<210> 18  
 <211> 26  
 <212> DNA  
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<220>  
 <223> oligonucleotide

<400> 18  
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26

<210> 19  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<400> 19  
 tttgtcgacg gtgagaggtc tagttc

26

<210> 20  
 <211> 72  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

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 atcctggagc gt

60

72



<210> 21  
 <211> 25  
 <212> PRT  
 <213> rat

<400> 21  
 Lys Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys  
   1                  5                  10                  15  
 Lys Ser Arg Phe Lys Ser Trp Ser Val  
                   20                  25

<210> 22  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide

<221> modified\_base  
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       h = t,c,a  
       y = t,c  
       r = a,g

<400> 22  
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26

<210> 23  
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 <212> DNA  
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<220>  
 <223> oligonucleotide

<221> modified\_base  
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       r = a,g

<400> 23  
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26

<210> 24  
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 <223> oligonucleotide

<400> 24

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<210> 25  
<211> 27  
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<210> 26  
<211> 26  
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<220>  
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<400> 26  
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<210> 27  
<211> 27  
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<220>

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26